CLAIMS

We claim:

1. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

2. The method of claim 1 wherein the primers are 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides long.

3. The method of claim 2 wherein the primers are 5, 6, 7, 8, 9, or 10 nucleotides long.

4. The method of claim 2 wherein the primers are 5, 6, 7, or 8 nucleotides long.

5. The method of claim 2 wherein the primers are 6, 7, or 8 nucleotides long.

6. The method of claim 2 wherein the primers are 6 nucleotides long.

7. The method of claim 1 wherein the primers each contain at least one modified nucleotide such that the primers are resistant to 3'-5' exonuclease.

8. The method of claim 1 wherein the DNA polymerase is bacteriophage ϕ29 DNA polymerase, Tts DNA polymerase, phage M2 DNA polymerase, VENT™ DNA polymerase, Klenow fragment of DNA polymerase I, T5 DNA polymerase, PRD1 DNA polymerase, T4 DNA polymerase holoenzyme, T7 native polymerase T7 Sequenase®, or Bst DNA polymerase.

9. The method of claim 8 wherein the DNA polymerase is ϕ29 DNA polymerase.

10. The method of claim 1 wherein the primers are 6 nucleotides long, wherein the primers each contain at least one modified nucleotide such that the primers are nuclease resistant, and wherein the DNA polymerase is ϕ29 DNA polymerase.

11. The method of claim 1 further comprising labeling the replicated strands using terminal deoxynucleotidyl transferase.

12. The method of claim 11 wherein the replicated strands are labeled by the addition of modified nucleotides to the replicated strands.

13. The method of claim 12 wherein the modified nucleotides are biotinylated nucleotides, fluorescent nucleotides, 5 methyl dCTP, BrdUTP, or 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates.

14. The method of claim 1 wherein modified nucleotides are incorporated into the replicated strands during replication.

15. The method of claim 14 wherein the modified nucleotides are biotinylated nucleotides, fluorescent nucleotides, 5 methyl dCTP, BrdUTP, or 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates.

16. The method of claim 15 wherein the modified nucleotides are 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates and wherein the replicated strands are labeled by reacting labels with the incorporated 5-(3-aminoallyl)-2'-deoxyuridines.

17. The method of claim 16 wherein the labels are fluorescein isothiocyanate, 5,6-carboxymethyl fluorescein, Texas red, nitrobenz-2-oxa-1,3-diazol-4-yl, coumarin, dansyl chloride, rhodamine, amino-methyl coumarin, Eosin, Erythrosin, BODIPY®, Cascade Blue®, Oregon Green®, pyrene, lissamine, xanthene, acridine, oxazines, phycoerythrin, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, or a combination thereof.

18. The method of claim 1 further comprising

diluting the replicated strands, bringing into contact a set of primers, DNA polymerase, and the diluted replicated strands, and incubating the replicated strands under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in additional replicated strands, wherein during replication at least one of the additional replicated strands is displaced from the target sequence by strand displacement replication of another additional replicated strand.

19. The method of claim 18 further comprising performing the following operation one or more times:

diluting the additional replicated strands, bringing into contact a set of primers, DNA polymerase, and the diluted replicated strands, and incubating the replicated strands under conditions that promote replication of the target sequence;

wherein replication of the target sequence results in additional replicated strands, wherein during replication at least one of the additional replicated strands is displaced from the target sequence by strand displacement replication of another additional replicated strand.

20. The method of claim 1 wherein the target sample is not subjected to heat denaturing conditions.

21. The method of claim 1 wherein the target sequence comprises two strands, wherein the set of primers has 3 or more primers complementary to one of the strands of the target sequence and at least one primer complementary to the other strand of the target sequence.

22. The method of claim 1 further comprising incubating the polymerase-target sample mixture under conditions that promote strand displacement.

23. The method of claim 1 wherein the set of primers has 3 or more primers complementary to the same strand of the target sequence.

24. The method of claim 1 wherein the set of primers has 4 or more primers complementary to the same strand of the target sequence.

25. The method of claim 1 wherein the set of primers has 4 or more primers.

26. The method of claim 25 wherein the set of primers has 5 or more primers.

27. The method of claim 1 wherein the conditions that promote replication of the target sequence are substantially isothermic.

28. The method of claim 1 wherein the conditions that promote replication of the target sequence do not involve thermal cycling.

29. The method of claim 1 wherein the conditions do not include thermal cycling.

30. The method of claim 1 wherein the target sequence comprises an amplification target and a hybridization target, wherein the hybridization target flanks the amplification target,

wherein the set of primers comprises a plurality of primers,

wherein each primer comprises a complementary portion, wherein the complementary portions of the primers are each complementary to a different portion of the hybridization target.

31. The method of claim 30 wherein the set of primers comprises a right set of primers and a left set of primers,

wherein the target sequence is double-stranded, having a first and a second strand,

wherein the hybridization target comprises a right and left hybridization target, wherein the right hybridization target flanks the amplification target on one end and the left hybridization target flanks the amplification target on the other end,

wherein the complementary portions of the right set primers are (i) all complementary to the first strand of the target sequence and (ii) each complementary to a different portion of the right hybridization target, and

wherein the complementary portions of the left set primers are (i) all complementary to the second strand of the target sequence and (ii) each complementary to a different portion of the left hybridization target.

32. The method of claim 31 wherein the right and left set of primers each have 3 or more primers.

33. The method of claim 32 wherein the right and left set of primers each have 4 or more primers.

34. The method of claim 33 wherein the right and left set of primers each have 5 or more primers.

35. The method of claim 31 wherein the right and left set of primers each have the same number of primers.

36. The method of claim 1 wherein the target sequence is a nucleic acid sample of substantial complexity, and wherein the set of primers comprises primers having random nucleotide sequences.

37. The method of claim 36 wherein the target sequence is a sample of genomic nucleic acid.

38. The method of claim 36 wherein the primers are from 5 to 20 nucleotides in length.

39. The method of claim 38 wherein the primers are from 5 to 10 nucleotides in length.

40. The method of claim 39 wherein the primers are 6, 7, or 8 nucleotides in length.

41. The method of claim 40 wherein the primers are 6 nucleotides in length.

42. The method of claim 36 wherein the primers are all of the same length.

43. The method of claim 36 wherein each primer comprises a constant portion and a random portion, wherein the constant portion of each primer has the same nucleotide sequence and the random portion of each primer has a random nucleotide sequence.

44. The method of claim 1 wherein the target sequence is concatenated DNA.

45. The method of claim 44 wherein the concatenated DNA is concatenated with linkers.

46. The method of claim 45 wherein each linker comprises a primer complement portion, wherein each primer comprises a complementary portion, wherein the complementary portion of each primer is complementary to the complementary portion of the linkers.

47. The method of claim 44 wherein the set of primers comprises primers having random nucleotide sequences.

48. The method of claim 47 wherein each primer comprises a constant portion and a random portion, wherein the constant portion of each primer has the same nucleotide sequence and the random portion of each primer has a random nucleotide sequence.

49. The method of claim 44 wherein the concatenated DNA is formed by ligating DNA fragments together.

50. The method of claim 49 wherein the DNA fragments are cDNA made from mRNA.

51. The method of claim 50 wherein the mRNA comprises a mixture of mRNA isolated from cells.

52. The method of claim 1 wherein the target sequence is not a nucleic acid molecule made up of multiple tandem repeats of a single sequence that was synthesized by rolling circle replication.

53. The method of claim 1 wherein the primers comprise nucleotides, wherein one or more of the nucleotides are ribonucleotides.

54. The method of claim 53 wherein from about 10% to about 50% of the nucleotides are ribonucleotides.

55. The method of claim 53 wherein about 50% or more of the nucleotides are ribonucleotides.

56. The method of claim 53 wherein all of the nucleotides are ribonucleotides.

57. The method of claim 1 wherein the primers comprise nucleotides, wherein one or more of the nucleotides are 2'-O-methyl ribonucleotides.

58. The method of claim 57 wherein from about 10% to about 50% of the nucleotides are 2'-O-methyl ribonucleotides.

59. The method of claim 57 wherein about 50% or more of the nucleotides are 2'-O-methyl ribonucleotides.

60. The method of claim 57 wherein all of the nucleotides are 2'-O-methyl ribonucleotides.

61. The method of claim 1 wherein the primers comprise nucleotides, wherein the nucleotides are a mixture of ribonucleotides and 2'-O-methyl ribonucleotides.

62. The method of claim 1 wherein the primers comprise nucleotides, wherein the nucleotides comprises bases, wherein one or more of the bases are universal bases.

63. The method of claim 62 wherein at least one of the universal bases is 3-nitropyrrole.

64. The method of claim 62 where the universal base is 5-nitroindole.

65. The method of claim 62 wherein from about 10% to about 50% of the bases are universal bases.

66. The method of claim 62 wherein about 50% or more of the bases are universal bases.

67. The method of claim 62 wherein all of the bases are universal bases.

68. The method of claim 1 wherein the target sample is a biopsy sample, a blood sample, a urine sample, a cell sample, or a tissue sample.

69. The method of claim 68 wherein the target sample is a needle aspiration biopsy sample.

70. The method of claim 68 wherein nucleic acids in the target sample are not separated from other material in the target sample.

71. The method of claim 68 wherein the target sample is a crude cell lysate.

72. The method of claim 68 wherein the target sample is not processed beyond cell lysis.

73. The method of claim 1 wherein the replicated strands are analyzed.

74. The method of claim 73 wherein the replicated strands are analyzed using one or more DNA chips.

75. The method of claim 73 wherein the replicated strands are analyzed by hybridization.

76. The method of claim 73 wherein the replicated strands are analyzed by nucleic acid sequencing.

77. The method of claim 73 wherein the replicated strands are stored prior to, following, or both prior to and following their analysis.

78. The method of claim 1 wherein the target sample is a blood sample, a urine sample, a semen sample, a lymphatic fluid sample, a cerebrospinal fluid sample, amniotic fluid sample, a biopsy sample, a needle aspiration biopsy sample, a cancer sample, a tumor sample, a tissue sample, a cell sample, a cell lysate sample, a crude cell lysate sample, a forensic sample, an archeological sample, an infection sample, a nosocomial infection sample, a production sample, a drug preparation sample, a biological molecule production sample, a protein preparation sample, a lipid preparation sample, a carbohydrate preparation sample, or a combination thereof.

79. The method of claim 78 wherein the target sample is a blood sample.

80. The method of claim 78 wherein the target sample is a needle aspiration biopsy sample.

81. The method of claim 78 wherein the target sample is a crude cell lysate sample.

82. The method of claim 78 wherein the target sample is a nosocomial infection sample.

83. The method of claim 82 wherein the sample is derived from a patient.

84. The method of claim 78 wherein the target sample is a biological molecule production sample.

85. The method of claim 84 wherein production of replicated strands indicates the presence of nucleic acids in the sample.

86. The method of claim 85 wherein the amount of replicated strands produced indicates the amount of nucleic acids in the sample.

87. The method of claim 78 wherein the target sample is a drug preparation sample.

88. The method of claim 78 wherein the target sample is a tumor sample.

89. The method of claim 78 wherein the target sample is amniotic fluid sample.

90. The method of claim 78 wherein the replicated strands produced from the target sample represent a nucleic acid fingerprint of the sample.

91. The method of claim 90 further comprising

bringing into contact a set of primers, DNA polymerase, and a second target sample, and incubating the second target sample under conditions that promote replication of the target sequence, wherein the second target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

92. The method of claim 91 wherein the second target sample is a sample from the same type of organism as the first target sample.

93. The method of claim 91 wherein the second target sample is a sample from the same type of tissue as the first target sample sample.

94. The method of claim 91 wherein the second target sample is a sample from the same organism as the first target sample.

95. The method of claim 94 wherein the second target sample is obtained at a different time than the first target sample.

96. The method of claim 91 wherein the second target sample is a sample from a different organism than the first target sample.

97. The method of claim 91 wherein the second target sample is a sample from a different type of tissue than the first target sample.

98. The method of claim 91 wherein the second target sample is a sample from a different species of organism than the first target sample.

99. The method of claim 91 wherein the second target sample is a sample from a different strain of organism than the first target sample.

100. The method of claim 91 wherein the second target sample is a sample from a different cellular compartment than the first target sample.

101. The method of claim 1 wherein a circular nucleic acid molecule comprises the target sequence.

102. The method of claim 101 wherein the circular nucleic acid molecule is produced by

digesting genomic DNA with a restriction endonuclease, and

circularizing the digested DNA.

103. The method of claim 102 wherein the digested DNA is circularized with DNA or RNA ligase.

104. The method of claim 102 wherein the digested DNA is circularized with a splint or adaptor.

105. The method of claim 102 wherein the target sequence comprises an amplification target and a hybridization target, wherein the hybridization target flanks the amplification target,

wherein the set of primers comprises a plurality of primers,

wherein each primer comprises a complementary portion, wherein the complementary portions of the primers are each complementary to a different portion of the hybridization target.

106. The method of claim 105 wherein the set of primers comprises a right set of primers and a left set of primers,

wherein the target sequence is double-stranded, having a first and a second strand,

wherein the hybridization target comprises a right and left hybridization target, wherein the right hybridization target flanks the amplification target on one end and the left hybridization target flanks the amplification target on the other end,

wherein the complementary portions of the right set primers are (i) all complementary to the first strand of the target sequence and (ii) each complementary to a different portion of the right hybridization target, and

wherein the complementary portions of the left set primers are (i) all complementary to the second strand of the target sequence and (ii) each complementary to a different portion of the left hybridization target.

107. The method of claim 101 wherein the circular nucleic acid molecule is produced by

circularizing cDNA.

108. The method of claim 101 wherein the circular nucleic acid molecule is produced by

circularizing mRNA/cDNA hybrid.

109. The method of claim 108 wherein the mRNA/cDNA hybrid is circularized with DNA or RNA ligase.

110. The method of claim 108 wherein the mRNA/cDNA hybrid is circularized with a splint or adaptor.

111. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein nucleic acids in the target sample are not separated from other material in the target sample,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

112. The method of claim 111 wherein the target sample is a crude cell lysate.

113. The method of claim 111 wherein the target sample is not processed beyond cell lysis.

114. The method of claim 111 wherein the target sample is a blood sample, a urine sample, a semen sample, a lymphatic fluid sample, a cerebrospinal fluid sample, amniotic fluid sample, a biopsy sample, a needle aspiration biopsy sample, a cancer sample, a tumor sample, a tissue sample, a cell sample, a cell lysate sample, a crude cell lysate sample, a forensic sample, an archeological sample, an infection sample, a nosocomial infection sample, a production sample, a drug preparation sample, a biological molecule production sample, a protein preparation sample, a lipid preparation sample, a carbohydrate preparation sample, or a combination thereof.

115. The method of claim 114 wherein the target sample is a blood sample.

116. The method of claim 114 wherein the target sample is a needle aspiration biopsy sample.

117. The method of claim 114 wherein the target sample is a crude cell lysate sample.

118. The method of claim 114 wherein the target sample is a nosocomial infection sample.

119. The method of claim 118 wherein the sample is derived from a patient.

120. The method of claim 114 wherein the target sample is a biological molecule production sample.

121. The method of claim 120 wherein production of replicated strands indicates the presence of nucleic acids in the sample.

122. The method of claim 121 wherein the amount of replicated strands produced indicates the amount of nucleic acids in the sample.

123. The method of claim 114 wherein the target sample is a drug preparation sample.

124. The method of claim 114 wherein the target sample is a tumor sample.

125. The method of claim 114 wherein the target sample is amniotic fluid sample.

126. The method of claim 114 wherein the replicated strands produced from the target sample represent a nucleic acid fingerprint of the sample.

127. The method of claim 126 further comprising

bringing into contact a set of primers, DNA polymerase, and a second target sample, and incubating the second target sample under conditions that promote replication of the target sequence, wherein the second target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

128. The method of claim 127 wherein the second target sample is a sample from the same type of organism as the first target sample.

129. The method of claim 127 wherein the second target sample is a sample from the same type of tissue as the first target sample sample.

130. The method of claim 127 wherein the second target sample is a sample from the same organism as the first target sample.

131. The method of claim 130 wherein the second target sample is obtained at a different time than the first target sample.

132. The method of claim 127 wherein the second target sample is a sample from a different organism than the first target sample.

133. The method of claim 127 wherein the second target sample is a sample from a different type of tissue than the first target sample.

134. The method of claim 127 wherein the second target sample is a sample from a different species of organism than the first target sample.

135. The method of claim 127 wherein the second target sample is a sample from a different strain of organism than the first target sample.

136. The method of claim 127 wherein the second target sample is a sample from a different cellular compartment than the first target sample.

137. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is a crude cell lysate,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

138. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the primers are 5, 6, 7, 8, 9, or 10 nucleotides long,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

139. The method of claim 138 wherein the set of primers comprises primers having random nucleotide sequences.

140. The method of claim 138 wherein the primers are 5, 6, 7, or 8 nucleotides long.

141. The method of claim 138 wherein the primers are 6, 7, or 8 nucleotides long.

142. The method of claim 138 wherein the primers are 6 nucleotides long.

143. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the primers each contain at least one modified nucleotide such that the primers are nuclease resistant,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

144. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target

sequence, wherein the primer-target sample is not subjected to denaturing conditions, wherein the primers are 6 nucleotides long, wherein the primers each contain at least one modified nucleotides such that the primers are nuclease resistant, and wherein DNA polymerase is ϕ29 DNA polymerase,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

145. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

diluting the replicated strands, bringing into contact a set of primers, DNA polymerase, and the diluted replicated strands, and incubating the replicated strands under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in additional replicated strands, wherein during replication at least one of the additional replicated strands is displaced from the target sequence by strand displacement replication of another additional replicated strand.

146. The method of claim 145 further comprising performing the following operation one or more times:

diluting the additional replicated strands, bringing into contact a set of primers, DNA polymerase, and the diluted replicated strands, and incubating the replicated strands under conditions that promote replication of the target sequence;

wherein replication of the target sequence results in additional replicated strands, wherein during replication at least one of the additional replicated strands is displaced from the target sequence by strand displacement replication of another additional replicated strand.

147. A method of amplifying a target nucleic acid sequence, the method comprising,

(a) mixing a set of primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the primers and the target sequence in the primer-target sample mixture, wherein the primer-target sample is not subjected to denaturing conditions,

(b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence,

wherein the set of primers comprises a right set of primers and a left set of primers,

wherein the target sequence is double-stranded, having a first and a second strand,

wherein the right set primers are all complementary to the first strand of the target sequence and the left set primers are all complementary to the second strand of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

148. The method of claim 147 wherein the right set of primers has 4 or more primers and the left set of primers has 4 or more primers.

149. A method of amplifying a target nucleic acid sequence, the method comprising,

(a) mixing a set of primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the primers and the target sequence in the primer-target sample mixture, wherein the primer-target sample is not subjected to denaturing conditions,

(b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

wherein the target sequence is a nucleic acid sample of substantial complexity, and wherein the set of primers comprises primers having random nucleotide sequences.

150. A method of amplifying a target nucleic acid sequence, the method comprising,

(a) mixing a set of primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the primers and the target sequence in the primer-target sample mixture, wherein the primer-target sample is not subjected to denaturing conditions,

(b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence,

wherein all of the primers in the set of primers are complementary to the same strand in the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

151. The method of claim 150 wherein the set of primers has 3 or more primers.

152. A method of amplifying a target nucleic acid sequence, the method comprising,

(a) mixing a set of primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the primers and the target sequence in the primer-target

sample mixture, wherein the primer-target sample is not subjected to denaturing conditions,

(b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

wherein the target sequence is a nucleic acid sample of substantial complexity, and wherein the set of primers comprises primers having random nucleotide sequences,

wherein each primer comprises a constant portion and a random portion, wherein the constant portion of each primer has the same nucleotide sequence and the random portion of each primer has a random nucleotide sequence.

153. A method of amplifying a target nucleic acid sequence, the method comprising,

(a) mixing a set of primers with a target sample, to produce a primer-target sample mixture, and incubating the primer-target sample mixture under conditions that promote hybridization between the primers and the target sequence in the primer-target sample mixture, wherein the primer-target sample is not subjected to denaturing conditions,

(b) mixing DNA polymerase with the primer-target sample mixture, to produce a polymerase-target sample mixture, and incubating the polymerase-target sample mixture under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

wherein the conditions that promote replication of the target sequence do not involve thermal cycling, and

wherein the target sequence is concatenated DNA.

154. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

155. The method of claim 154 wherein the set of primers has 3 or more primers complementary to the same strand of the target sequence.

156. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand, wherein the target sequence is a nucleic acid sample of substantial complexity, and wherein the set of primers comprises primers having random nucleotide sequences.

157. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to denaturing conditions,

wherein all of the primers in the set of primers are complementary to the same strand in the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

158. The method of claim 157 wherein the set of primers has 3 or more primers.

159. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

wherein the target sequence is a nucleic acid sample of substantial complexity, and wherein the set of primers comprises primers having random nucleotide sequences,

wherein each primer comprises a constant portion and a random portion, wherein the constant portion of each primer has the same nucleotide sequence and the random portion of each primer has a random nucleotide sequence.

160. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

wherein the conditions that promote replication of the target sequence do not involve thermal cycling, and

wherein the target sequence is concatenated DNA.

161. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein the target sample is not subjected to heat denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

162. A method of labeling nucleic acids produced by strand displacement replication, the method comprising

labeling nucleic acids produced by strand displacement replication using terminal deoxynucleotidyl transferase.

163. The method of claim 162 wherein the replicated strands are labeled by the addition of modified nucleotides to the 3' ends of the nucleic acids.

164. The method of claim 163 wherein the modified nucleotides are biotinylated nucleotides, fluorescent nucleotides, 5 methyl dCTP, BrdUTP, or 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates.

165. A method of labeling nucleic acids produced by strand displacement replication, the method comprising

incorporating modified nucleotides into nucleic acids produced by strand displacement replication during replication.

166. The method of claim 165 wherein the modified nucleotides are biotinylated nucleotides, fluorescent nucleotides, 5 methyl dCTP, BrdUTP, or 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates.

167. The method of claim 166 wherein the modified nucleotides are 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates and wherein the replicated strands are labeled by reacting labels with the incorporated 5-(3-aminoallyl)-2'-deoxyuridines.

168. The method of claim 167 wherein the labels are fluorescein isothiocyanate, 5,6-carboxymethyl fluorescein, Texas red, nitrobenz-2-oxa-1,3-diazol-4-yl, coumarin, dansyl chloride, rhodamine, amino-methyl coumarin, Eosin, Erythrosin, BODIPY®, Cascade Blue®, Oregon Green®, pyrene, lissamine, xanthene, acridine, oxazines, phycoerythrin, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, or a combination thereof.

169. A method of attaching nucleic acids produced by strand displacement replication, the method comprising

adding modified nucleotides to the 3' ends of nucleic acids produced by strand displacement replication using terminal deoxynucleotidyl transferase, and

reacting the modified nucleotides with a solid-state support thereby attaching the nucleic acids to the solid-state support.

170. A microarray comprising nucleic acids produced by strand displacement replication coupled or adhered to a solid-state substrate.

171. A method of generating probes based on a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand,

wherein the replicated strands are used as hybridization probes.

172. The method of claim 171 wherein the replicated strands are used as elements in a microarray.

173. The method of claim 171 wherein the replicated strands are cleaved prior to use as hybridization probes.

174. The method of claim 173 wherein the replicated strands are cleaved with DNAse I.

175. The method of claim 171 further comprising labeling the hybridization probes using terminal deoxynucleotidyl transferase.

176. The method of claim 175 wherein the hybridization probes are labeled by the addition of modified nucleotides to the 3' ends of the replicated strands.

177. The method of claim 176 wherein the modified nucleotides are reacted with a solid-state support thereby attaching the replicated strands to the solid-state support.

178. The method of claim 176 wherein the modified nucleotides are biotinylated nucleotides, fluorescent nucleotides, 5 methyl dCTP, BrdUTP, or 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates.

179. The method of claim 171 wherein modified nucleotides are incorporated into the replicated strands during replication.

180. The method of claim 179 wherein the modified nucleotides are biotinylated nucleotides, fluorescent nucleotides, 5 methyl dCTP, BrdUTP, or 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates.

181. The method of claim 180 wherein the modified nucleotides are 5-(3-aminoallyl)-2'-deoxyuridine 5'-triphosphates and wherein the replicated strands are labeled by reacting labels with the incorporated 5-(3-aminoallyl)-2'-deoxyuridines.

182. The method of claim 181 wherein the labels are fluorescein isothiocyanate, 5,6-carboxymethyl fluorescein, Texas red, nitrobenz-2-oxa-1,3-diazol-4-yl, coumarin, dansyl chloride, rhodamine, amino-methyl coumarin, Eosin, Erythrosin, BODIPY®, Cascade Blue®, Oregon Green®, pyrene, lissamine, xanthene, acridine, oxazines, phycoerythrin, Cy3, Cy3.5, Cy5, Cy5.5, Cy7, or a combination thereof.

183. A method of amplifying messenger RNA, the method comprising,

reverse transcribing messenger RNA to produce a first strand cDNA,

bringing into contact a set of primers, DNA polymerase, and the first strand cDNA, and incubating under conditions that promote replication of the first strand cDNA,

wherein replication of the first strand cDNA results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the first strand cDNA by strand displacement replication of another replicated strand.

184. The method of claim 183 further comprising, prior to replication, degrading the messenger RNA using RNAse H.

185. The method of claim 183 wherein the target sample is a blood sample, a urine sample, a semen sample, a lymphatic fluid sample, a cerebrospinal fluid sample, amniotic fluid sample, a biopsy sample, a needle aspiration biopsy sample, a cancer sample, a tumor sample, a tissue sample, a cell sample, a cell lysate sample, a crude cell lysate sample, a forensic sample, an archeological sample, an infection sample, a nosocomial infection sample, a production sample, a drug preparation sample, a biological molecule production sample, a protein preparation sample, a lipid preparation sample, a carbohydrate preparation sample, or a combination thereof.

186. The method of claim 185 wherein the target sample is a blood sample.

187. The method of claim 185 wherein the target sample is a needle aspiration biopsy sample.

188. The method of claim 185 wherein the target sample is a crude cell lysate sample.

189. The method of claim 185 wherein the target sample is a nosocomial infection sample.

190. The method of claim 189 wherein the sample contains both human and non-human nucleic acids.

191. The method of claim 190 wherein the non-human nucleic acid is amplified preferentially by the use of primers specific for the non-human nucleic acid.

192. The method of claim 190 wherein the human nucleic acid is amplified preferentially by the use of primers specific for human nucleic acid.

193. The method of claim 189 wherein the sample is derived from a patient.

194. The method of claim 185 wherein the target sample is a biological molecule production sample.

195. The method of claim 194 wherein production of replicated strands indicates the presence of nucleic acids in the sample.

196. The method of claim 195 wherein the amount of replicated strands produced indicates the amount of nucleic acids in the sample.

197. The method of claim 185 wherein the target sample is a drug preparation sample.

198. The method of claim 185 wherein the target sample is a tumor sample.

199. The method of claim 185 wherein the target sample is amniotic fluid sample.

200. The method of claim 185 wherein the replicated strands produced from the target sample represent a nucleic acid fingerprint of the sample.

201. The method of claim 200 further comprising

bringing into contact a set of primers, DNA polymerase, and a second target sample, and incubating the second target sample under conditions that promote replication of the target sequence, wherein the second target sample is not subjected to denaturing conditions,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

202. The method of claim 201 wherein the second target sample is a sample from the same type of organism as the first target sample.

203. The method of claim 201 wherein the second target sample is a sample from the same type of tissue as the first target sample sample.

204. The method of claim 201 wherein the second target sample is a sample from the same organism as the first target sample.

205. The method of claim 204 wherein the second target sample is obtained at a different time than the first target sample.

206. The method of claim 201 wherein the second target sample is a sample from a different organism than the first target sample.

207. The method of claim 201 wherein the second target sample is a sample from a different type of tissue than the first target sample.

208. The method of claim 201 wherein the second target sample is a sample from a different species of organism than the first target sample.

209. The method of claim 201 wherein the second target sample is a sample from a different strain of organism than the first target sample.

210. The method of claim 201 wherein the second target sample is a sample from a different cellular compartment than the first target sample.

211. A method of amplifying a target nucleic acid sequence, the method comprising,

partially degrading RNA in a target sample,

bringing into contact DNA polymerase, and the target sample, and incubating the target sample under conditions that promote replication of the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

212. A method of comparative genome hybridization, the method comprising,

hybridizing nucleic acids produced by strand displacement replication of a first sample with nucleic acids produced by strand displacement replication of a second sample.

213. The method of claim 212 wherein hybridization is carried out in the absence of CotI DNA.

214. A method of amplifying a target nucleic acid sequence, the method comprising,

bringing into contact a set of primers, DNA polymerase, and a target sample, and incubating the target sample under conditions that promote replication of the target sequence, wherein a circular nucleic acid molecule comprises the target sequence,

wherein replication of the target sequence results in replicated strands, wherein during replication at least one of the replicated strands is displaced from the target sequence by strand displacement replication of another replicated strand.

215. The method of claim 214 wherein the circular nucleic acid molecule is produced by

digesting genomic DNA with a restriction endonuclease, and

circularizing the digested DNA.

216. The method of claim 215 wherein the digested DNA is circularized with DNA or RNA ligase.

217. The method of claim 215 wherein the digested DNA is circularized with a splint or adaptor.

218. The method of claim 215 wherein the target sequence comprises an amplification target and a hybridization target, wherein the hybridization target flanks the amplification target,

wherein the set of primers comprises a plurality of primers,

wherein each primer comprises a complementary portion, wherein the complementary portions of the primers are each complementary to a different portion of the hybridization target.

219. The method of claim 218 wherein the set of primers comprises a right set of primers and a left set of primers,

wherein the target sequence is double-stranded, having a first and a second strand,

wherein the hybridization target comprises a right and left hybridization target, wherein the right hybridization target flanks the amplification target on one end and the left hybridization target flanks the amplification target on the other end,

wherein the complementary portions of the right set primers are (i) all complementary to the first strand of the target sequence and (ii) each complementary to a different portion of the right hybridization target, and

wherein the complementary portions of the left set primers are (i) all complementary to the second strand of the target sequence and (ii) each complementary to a different portion of the left hybridization target.

220. The method of claim 214 wherein the circular nucleic acid molecule is produced by

circularizing cDNA.

221. The method of claim 214 wherein the circular nucleic acid molecule is produced by

circularizing mRNA/cDNA hybrid.

222. The method of claim 221 wherein the mRNA/cDNA hybrid is circularized with DNA or RNA ligase.

223. The method of claim 221 wherein the mRNA/cDNA hybrid is circularized with a splint or adaptor.